Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of the Claims

1. (Previously Presented) A recognition system comprising:

(a) at least one immobilized capture sequence having at least one binding site for a complementary recognition sequence, wherein the capture sequence is selected from the group consisting of pyranosyl nucleic acid (p-NA) and nucleic acid having one or more aminocyclohexylethanoic acid (CNA) units; and

(b) at least one complementary recognition sequence that binds to the capture sequence and contains at least one binding site for a substrate S, wherein the recognition sequence is selected from the group consisting of pyranosyl nucleic acid (p-NA) and nucleic acid having one or more aminocyclohexylethanoic acid (CNA) units, and wherein the binding of the capture sequence to the recognition sequence forms a molecular pairing system.

2. (Previously Presented) The recognition system according to claim 1, wherein the molecular pairing system is a complex that is formed by association of the capture sequence with the complementary recognition sequence via non-covalent interactions.

3. (Previously Presented) The recognition system according to claim 2, wherein the non-covalent interactions are selected from the group consisting of hydrogen bridges, salt bridges, stacking, metal ligands, charge-transfer complexes, and hydrophobic interactions.

4-7. (Canceled)

8. (Previously Presented) The recognition system according to claim 1, wherein at least one nucleobase of the capture or recognition sequences is selected from the group consisting of purine, 2,6-diaminopurine, 6-purinethiol, pyridine, pyrimidine, adenine, guanine, isoguanine, 6-

thioguanine, xanthine, hypoxanthine, thymine, cytosine, isocytosine, indole, tryptamine, N-phthaloyltryptamine, uracil, caffeine, theobromine, theophylline, benzotriazole, and acridine.

9. (Previously Presented) The recognition system according to claim 1, wherein the p-NA is selected from the group consisting of ribopyranosyladenosine, ribopyranosylguanosine, ribopyranosylthymidine, ribopyranosylcytosine, ribopyranosyltryptamine or ribopyranosyl-N-phthalotryptamine, ribopyranosyluracil, and their 2-amino-4-(carboxymethyl)ribopyranosyl derivatives.

10. (Previously Presented) The recognition system according to claim 1, wherein the length of the capture or recognition sequences are at least about 4-50 nucleotides.

11. (Previously Presented) The recognition system according to claim 1, wherein the capture sequence is immobilized on a carrier.

12. (Previously Presented) The recognition system according to claim 11, wherein the carrier is selected from the group consisting of ceramic, metal, glasses, polymers, and crystalline materials.

13. (Previously Presented) The recognition system according to claim 11, wherein the capture sequence is immobilized on the carrier by means of a covalent bond, quasi-covalent bond or supramolecular bond by association of two or more molecular species.

14. (Previously Presented) The recognition system according to claim 11, wherein the capture sequence is immobilized at defined sites of the carrier.

15. (Previously Presented) The recognition system according to claim 14, wherein the defined sites of the carrier are addressed.

16. (Previously Presented) The recognition system according to claim 11, wherein the capture sequence is immobilized on a carrier electrode of the carrier.

17. (Previously Presented) The recognition system according to claim 1, wherein the binding site is a biomolecule that binds substrate S.

18. (Previously Presented) The recognition system according to claim 17, wherein the biomolecule is selected from the group consisting of peptides, peptoids, proteins, lipids, glycoproteins, filament constituents, viruses, viroids, saccharides, nucleic acids, and their active moieties.

19. (Previously Presented) The recognition system according to claim 1, wherein the immobilized capture sequence contains various binding sites for the complementary recognition sequence, by means of which various complementary recognition sequences bind to the capture sequence.

20. (Previously Presented) The recognition system according to claim 1, wherein at least one further complementary recognition sequence is bound to the capture sequence.

21-23. (Cancelled)

24. (Previously Presented) The recognition system according to claim 34, wherein the various biomolecules bind the substrate S.

25. (Previously Presented) The recognition system according to claim 24, wherein the substrate S is selected from the group consisting of peptides, peptoids, proteins, lipids, glycoproteins, filament constituents, viruses, viroids, saccharides, nucleic acids, and their active moieties.

26. (Previously Presented) The recognition system according to claim 1, wherein the at least one binding site for substrate S comprises antibodies, antibody fragments, and derivatives thereof.

27. (Previously Presented) A process for identifying a substrate S in a sample, the process comprising:

(a) providing a recognition system comprising:

at least one immobilized capture sequence having at least one binding site for a complementary recognition sequence, wherein the capture sequence is selected from the group consisting of pyranosyl nucleic acid (p-NA) and nucleic acid having one or more aminocyclohexylethanoic acid (CNA) units; and

at least one complementary recognition sequence that binds to the capture sequence and contains at least one binding site for a substrate S, wherein the recognition sequence is selected from the group consisting of pyranosyl nucleic acid (p-NA) and nucleic acid having one or more aminocyclohexylethanoic acid (CNA) units, and wherein the binding of the capture sequence to the recognition sequence forms a molecular pairing system;

(b) contacting the recognition sequence containing at least one binding site for substrate S with a sample containing substrate S;

(c) simultaneously or successively contacting the recognition sequence and sample with the immobilized capture sequence to form an immobilized complex; and

(d) detecting a complex of immobilized capture sequence, recognition sequence, and substrate S.

28. (Previously Presented) The process according to claim 27, wherein the formation of the complex is controlled by means of physical parameters.

29. (Previously Presented) The process according to claim 27, wherein the complex is detected by means of a label on the complex or by directly detecting the complex itself.

30. (Previously Presented) The process according to claim 27, further comprising isolating the complex of the recognition sequence and substrate S.

31. (Previously Presented) The process according to claim 27, wherein the complex of recognition sequence and substrate S is in a binding equilibrium, and further comprising isolating the complex after freezing the binding equilibrium.

32. (Canceled)

33. (Previously Presented) The process according to claim 30, further comprising the step of covalently cross-linking the recognition sequence and substrate S.

34. (Previously Presented) The recognition system according to claim 20, wherein the binding site of at least one further complementary recognition sequence is an additional biomolecule.

35. (Previously Presented) The recognition system according to claim 1, wherein the length of the capture or recognition sequences is at least about 4-25 nucleotides.

36. (Previously Presented) The recognition system according to claim 1, wherein the length of the capture or recognition sequences is at least about 4-15 nucleotides.

37. (Previously Presented) The recognition system according to claim 1, wherein the length of the capture or recognition sequences is at least about 4-10 nucleotides.

38. (Previously Presented) The recognition system according to Claim 11, wherein the carrier comprises a noble metal.

39. (Previously Presented) The recognition system according to Claim 11, wherein the carrier comprises a (bio)molecule polymer.

40. (Previously Presented) The recognition system according to Claim 11, wherein the carrier comprises a structural protein.

41. (Previously Presented) The recognition system according to Claim 13, wherein the two or more molecular species are selected from a group consisting of peptides, peptoids, proteins, linear oligo- or polysaccharides, nucleic acids, heterocycles, branched oligo- or polysaccharides, antibodies, and derivatives thereof.

42. (Previously Presented) The recognition system according to Claim 1, wherein the p-NA is a pyranosyl-RNA (p-RNA).

43. (Previously Presented) The recognition system according to claim 11, wherein the capture sequence is immobilized at defined sites of the carrier in a matrix.

44. (Previously Presented) The process of claim 28, wherein the physical parameters are selected from the group consisting of temperature, salts, solvents, and electrophoretic processes.

45. (Previously Presented) The process according to Claim 29, wherein the complex is detected by means of radioactive labeling, fluorescent labeling, enzymatic labeling, redox labeling, spin labeling of the recognition sequence, redox processes in an environment or on an electrode, impedance measurement, or direct current measurement.

46-64. (Canceled)